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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

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Reviewer: markspencer

Timestamp: [year=2008; month=5; day=2; hr=15; min=36; sec=47; ms=445; ]

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Reviewer Comments:

Remove the "10" at the end of the file after SEQ ID # 22. Also remove the blank <223> in SEQ ID # 1 and 3.

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Application No: 10573478 Version No: 2.0

**Input Set:**

**Output Set:**

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**Finished:** 2008-04-17 15:51:28.390  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 623 ms  
**Total Warnings:** 6  
**Total Errors:** 4  
**No. of SeqIDs Defined:** 22  
**Actual SeqID Count:** 22

Error code	Error Description
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
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W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)

SEQUENCE LISTING

<110> Kiselev, Vsevolod I  
Petr, Sveshnikov G

<120> METHODS, KITS, AND COMPOSITIONS FOR THE DEVELOPMENT AND USE  
OF MONOCLONAL ANTIBODIES SPECIFIC TO ANTIGENS TRADITIONALLY  
OF LOW IMMUNOGENICITY

<130> Immunize

<140> 10573478  
<141> 2008-04-17

<150> RU 2003128660  
<151> 2003-09-25

<160> 22

<170> PatentIn version 3.1

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<212> DNA  
<213> Human papillomavirus type 16

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Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn  
15 20 25 30

gac agc tca gag gag gat gaa ata gat ggt cca gct gga caa gca 144  
Asp Ser Ser Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala  
35 40 45

gaa ccg gac aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt 192  
Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys  
50 55 60

gac tct acg ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt 240  
Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg  
65 70 75

act ttg gaa gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc 288  
Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile  
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tgt tct cag aaa cca ggatcc 309

Cys Ser Gln Lys Pro

95

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35 40 45

Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser  
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Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu  
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His Leu Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu

15 20 25 30

caa tta agc gac tca gag gaa gaa aac gat gaa ata gat gga gtt aat 144

Gln Leu Ser Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn

35 40 45

cat caa cat tta cca gcc cga cga gct gaa cca caa cgt cac aca atg 192  
His Gln His Leu Pro Ala Arg Arg Ala Glu Pro Gln Arg His Thr Met  
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ttg tgt atg tgt tgt aag tgt gaa gcc aga att gag cta gta gta gaa 240  
Leu Cys Met Cys Cys Lys Cys Glu Ala Arg Ile Glu Leu Val Val Glu  
65 70 75

agc tca gca gac gac ctt cga gca ttc cag cag ctg ttt ctg aac acc 288  
Ser Ser Ala Asp Asp Leu Arg Ala Phe Gln Gln Leu Phe Leu Asn Thr  
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35 40 45

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